



SEQUENCE LISTING

<110> GIORGI, DOMINIQUE
SAFFIN, JEAN-MICHEL
ROUQUIER, SYLVIE

<120> NOVEL CENTROSOME-ASSOCIATED PROTEIN AND APPLICATIONS
THEREOF

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<140> 10/540,493
<141> 2005-06-24

<150> PCT/FR03/003895
<151> 2003-12-24

<150> FR 02 16648
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<170> PatentIn Ver. 3.3

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 ggtaccataa tgatagaaat tattcctttt gtggatgatt gtgaatctag attcagggtt 29700
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<210> 17
 <211> 200
 <212> DNA
 <213> Homo sapiens

<400> 17
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 cccgagagac cccgcgggtgg ggaagtcact tcctcccgaa gacgctgttt cctagcaacc 120
 gcccctccgccc tctgttattt gcccctccctc ctcgctcggc ccaggaccgg ctctgcggg 180
 gccgcaggc ccagaccaag 200

<210> 18
 <211> 139
 <212> DNA
 <213> Homo sapiens

<400> 18
 ctactatcg aagttgaatt ctaataatta gctattttat aaaggtaacg agaaaaaaaata 60
 cactatgtct gatgaagttt ttagcaccac tttggcatat acaaagagtc caaaagttac 120
 caaaagaact actttccag 139

<210> 19
 <211> 85
 <212> DNA
 <213> Homo sapiens

<400> 19
 gatgagctaa taagagcaat tacagctcgc tcagccagac aaaggagttc tgaatactca 60
 gatgactttg acagtgtatgatgatgattt 85

<210> 20
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 20
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 atgactttca tatatcagat gatgaagaaa agaattccttc aaaactattt gtttgaaaaa 120

ccaataaaatc aaacggtaac ataaccaaag atgagccagt gtgtgccatc aaaaatgaag 180
 agggaaatggc acctgatggg tgtgaagaca ttgttgtaaa atcttctct gaatctcaa 240
 ataaggatga ggaatttcaa aaagacaaaa taaaaatgaa acctaaaccc agaattctt 300
 caattaaaag cacatcttca g 321

<210> 21
 <211> 227
 <212> DNA
 <213> Homo sapiens

<400> 21
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 tggaaaaaa gaaaagtcac atggaggaga aggtatggact agaagataaa gaaactgccc 120
 tcagtgaaatcatttgcac cttttccct tccaaacgccc aatggcatac 180
 aattagaagc tgagaaaaaa gcatttcttgaaaaccttga tcctgag 227

<210> 22
 <211> 94
 <212> DNA
 <213> Homo sapiens

<400> 22
 gattcatgtc taacaagtct agcatcatca tcacttaaac aaattcttgg agattcttt 60
 tcaccaggat ctgagggaaa cgcacatcgaa aaag 94

<210> 23
 <211> 248
 <212> DNA
 <213> Homo sapiens

<400> 23
 atccaaatga agaaatcaact gaaaaccata attccttggaa atcagatgaa aataaaagaga 60
 attcatatttc agcagaccat gtgactactg cagttgagaa atccaaaggaa agtcaagtga 120
 ctgctgtga ctttgaagaa gaaaaggcaa aagcggaaact gattatggat gatgacagaa 180
 cagttgtatcc actactatct aaatctcaga gtatcttaat atctaccatg gcaacagcat 240
 cttcaaag 248

<210> 24
 <211> 71
 <212> DNA
 <213> Homo sapiens

<400> 24
 aaaacaattt gaaatgaaaa tataaagaat aaaaagtcaa caaataatag agcatccagt 60
 gcatctgcca g 71

<210> 25
 <211> 169
 <212> DNA
 <213> Homo sapiens

<400> 25
 attaatgacc tctgagttt tgaagaaatc tagttctaaa aggagaactc catcgacaac 60

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tacctcttct cactatttag ggactttaaa agtcttggac caaaaacctt cacagaaaaca 120
gagcatagaa cctgtatagag cagataacat aagggcagct gtttatcag 169
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<210> 26
<211> 90
<212> DNA
<213> *Homo sapiens*

<400> 26
gagtggtag aaaaagaaaaa tgtgtattta catgaaatgc acagaataaa aagaattgaa 60
agtqaaaact taaqgatcca aaatqaacag 90

<210> 27
<211> 160
<212> DNA
<213> *Homo sapiens*

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<400> 27
aaaaaaagctg ctaaaagaga agaaggcatta gcatcatttgcggcctggaa ggctatgaaa 60
gaaaaggaaag caaagaaaaat agctgcctaaa aagaggcttgcggaaaaaa caagaagaaa 120
actqaaqaaqaaaatqctqc aqaaaaaqqa qaaqcactac 160
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<210> 28
<211> 146
<212> DNA
<213> *Homo sapiens*

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<400> 28
gctttgaaa aatggaaaga gaaaaagatg gaatatctta aagagaaaaaa tagaaaggag 60
agagaatatg aaagagcaaa gaaacagaaa gaggaggaaa ctgttgccga gaaaaagaaa 120
qataattaa ctqctqttqa qaaatq 146
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<210> 29
<211> 133
<212> DNA
<213> *Homo sapiens*

<400> 29
gaataaaaaa aaggaagctt ttttcaagca aaaggaaaaaa gaaaaaataa atgagaaaag 60
aaaggaagaa ctgaaaagag ctgagaaaaa agataaagat aaacaagcta ttaatgaata 120
tqaaaaatqq ctq 133

<210> 30
<211> 485
<212> DNA
<213> *Homo sapiens*

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<400> 30
gaaaataagg aaaaacaaga aagaattgaa cgaaaacaga agaaaacgtca ttcctttctt 60
gaaagtgagg cacttcctcc gtggagccct ccaagcagaa ctgtgttcgc aaaagtgttt 120
tgataattct agttcttaca ttatgggtt atttatcggt ttgccaatat tagccataga 180
tttaaaacca ttcaattatt tatagttaga ggaatatatt ttaattaaat gccagacact 240
cctgctgaca atqaaagaaa tactttggaa tctaattcagt gaaagcattt tttgaactg 300
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tagataaaact gcctcaaaca aagaccta aatcagattt ttttaccat taagatacat 360
 aagattttat catgtcctga taattctt ggtggagtga ttcatgatct ttttcattaa 420
 gctctgtatg ttatthaagt atattaattt ccagtaataa aaagggaaatc atcttaggtac 480
 cataa 485

<210> 31
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 31
 atgtctgatg aagtttttag cacc 24

<210> 32
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 32
 aggcctcaaa tgatgctaat gc 22

<210> 33
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 33
 atcatttgag gcctggaagg c 21

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 34
 aaacactttt gcgaacacag ttc 23

<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 35
 acaacgaata acagagtgtc c

21

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 36
 actccctgata aacagctgcc

20

<210> 37
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 37
 gccaccatgt ctgatgaagt ttttagcac

29

<210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 38
 gaaacacttt tgcgAACACA gttc

24

<210> 39
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 39
 taatgtctga tgaagttttt agcacc

26

<210> 40
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 40
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26

<210> 41
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 41
 aatgtctgat gaagttttta gcacc

25

<210> 42
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 42
 tcagcttgcc gtaggtggc

19

<210> 43
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 43
 atggtcctgc tggagttcg

19

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<210> 44
<211> 391
<212> DNA
<213> Mus musculus

<400> 44
aaagaagtga agacagaaaac acgaagaata aaaagacaac gaataacaga gtgtccagtg 60
cctctggcag gctgatgacc tctgagttt taaagagatc cggcccaca aaaagaagtc 120
catctgcagc tacccctca cactattag ggagttgaa agtcttggac cagaagcaac 180
cacgaaagca gaggccttagag ccagacaagg ctgatcacat aagggcagct gtttatcagg 240
agtggtaga aaagaaaaat gtgtattac atgaaatgca cagaataaaa agaattgaaa 300
gcgaaaacctt gaggatccaa aatgaacaga aaaaagctgc taagagagag gaagccctgg 360
catcattga ggcctgaaag gcaatgaaag a 391

<210> 45
<211> 2767
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (204)..(2147)

<400> 45
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agcaaccgccc ttctgcctcc atctttgcc ccgcctccag gttattccaa tacctggttt 120
cccagaccgc gaggccccggg ccggggggcga cacctgtgct agagcatagc cgctgggttc 180
tcagcagaga aaaaggacac acc atg tcc gat gaa atc ttc agc aca act ttg 233
Met Ser Asp Glu Ile Phe Ser Thr Thr Leu
1 5 10

gcg tac acc aag agt cca aag gct acc aag aga act tcc ttt cag gat 281
Ala Tyr Thr Lys Ser Pro Lys Ala Thr Lys Arg Thr Ser Phe Gln Asp
15 20 25

gag ctg atc aga gcc att aca gcc cgg tca gcc agg cag aga agt tcc 329
Glu Leu Ile Arg Ala Ile Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser
30 35 40

gaa tac tcc gat gac ttt gac agt gac gag att gtt tct tta ggt gaa 377
Glu Tyr Ser Asp Asp Phe Asp Ser Asp Glu Ile Val Ser Leu Gly Glu
45 50 55

ttt tca gat acc tcg aca gat gaa agt cta gtt aga aaa aag atg aat 425
Phe Ser Asp Thr Ser Thr Asp Glu Ser Leu Val Arg Lys Lys Met Asn
60 65 70

gat ttt cat ata tcc gac gat gag gaa aaa aat tct cca aga ctg tct 473
Asp Phe His Ile Ser Asp Asp Glu Glu Lys Asn Ser Pro Arg Leu Ser
75 80 85 90

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ttt ttg aaa acc aag aaa gta aac agg gca ata tcc aac gat gct ctg	521
Phe Leu Lys Thr Lys Lys Val Asn Arg Ala Ile Ser Asn Asp Ala Leu	
95 100 105	
gac tcc agc act ccg ggc agc gaa ggc tcg tca ccg gat gct caa gaa	569
Asp Ser Ser Thr Pro Gly Ser Glu Gly Ser Ser Pro Asp Ala Gln Glu	
110 115 120	
gat gtg act gga gat tcc ctc ccc aaa tct caa aat gat gat cga gaa	617
Asp Val Thr Gly Asp Ser Leu Pro Lys Ser Gln Asn Asp Asp Arg Glu	
125 130 135	
gtc ggc aga gag atc atc aca gtg aag cct aca ccc agg atg cac ccc	665
Val Gly Arg Glu Ile Ile Thr Val Lys Pro Thr Pro Arg Met His Pro	
140 145 150	
gtc aaa aga agc acg tcc tcg ggg gaa acc agc agc ggt ctt gat gca	713
Val Lys Arg Ser Thr Ser Ser Gly Glu Thr Ser Ser Gly Leu Asp Ala	
155 160 165 170	
gat ggc cac ttt aag cct tca ccc cag cca agg agc atg tta aaa aag	761
Asp Gly His Phe Lys Pro Ser Pro Gln Pro Arg Ser Met Leu Lys Lys	
175 180 185	
agc agc cac act gag gag gga gtc aga cca gga gtt gat aaa gaa cat	809
Ser Ser His Thr Glu Glu Gly Val Arg Pro Gly Val Asp Lys Glu His	
190 195 200	
tcc ata agc gaa gcc tct gct ccc aca cct tcc ctt cca agg cag aat	857
Ser Ile Ser Glu Ala Ser Ala Pro Thr Pro Ser Leu Pro Arg Gln Asn	
205 210 215	
ggc aca gag ttg caa act gag gaa aaa ata tac tcg gaa aac ctc gat	905
Gly Thr Glu Leu Gln Thr Glu Glu Lys Ile Tyr Ser Glu Asn Leu Asp	
220 225 230	
ctt gag gac tca ctc tta caa agt ctg acc tca tct tcc ttc aaa gaa	953
Leu Glu Asp Ser Leu Leu Gln Ser Leu Thr Ser Ser Ser Phe Lys Glu	
235 240 245 250	
agc ccc gga ggt tgc aca tca cca gga tct cag gaa aag gtg ccc ata	1001
Ser Pro Gly Gly Cys Thr Ser Pro Gly Ser Gln Glu Lys Val Pro Ile	
255 260 265	
aaa gat cat gat gga gaa cct act gaa atc tgg gat tcc ttg cta tca	1049
Lys Asp His Asp Gly Glu Pro Thr Glu Ile Trp Asp Ser Leu Leu Ser	
270 275 280	
aat gaa aat gaa gga agt tct gtt ttg gtg aac tgt gtt act cct gaa	1097
Asn Glu Asn Glu Gly Ser Ser Val Leu Val Asn Cys Val Thr Pro Glu	
285 290 295	
ctc gag cag ccc aag gac ggt cag gtg gca gct gac gac ctt gag gaa	1145
Leu Glu Gln Pro Lys Asp Gly Gln Val Ala Ala Asp Asp Leu Glu Glu	
300 305 310	

gaa aga gag aag ggt gga ttt aca gaa gat gac ctc acc act gac ccg	1193
Glu Arg Glu Lys Gly Gly Phe Thr Glu Asp Asp Leu Thr Thr Asp Pro	
315 320 325 330	
ctg ctc tcc acg tcc ccg agt gtc ata aca ccc act gag cca gca gag	1241
Leu Leu Ser Thr Ser Pro Ser Val Ile Thr Pro Thr Glu Pro Ala Glu	
335 340 345	
ccg gcc aag aaa gca aat gaa gac aga aac acg aag aat aaa aag aca	1289
Pro Ala Lys Lys Ala Asn Glu Asp Arg Asn Thr Lys Asn Lys Lys Thr	
350 355 360	
acg aat aac aga gtg tcc agt gcc tct ggc agc agg ctg atg acc tct	1337
Thr Asn Asn Arg Val Ser Ser Ala Ser Gly Ser Arg Leu Met Thr Ser	
365 370 375	
gag ttt tta aag aga tcc ggt ccc aca aaa aga agt cca tct gca gct	1385
Glu Phe Leu Lys Arg Ser Gly Pro Thr Lys Arg Ser Pro Ser Ala Ala	
380 385 390	
acc tcc tca cac tat tta ggg agt ttg aaa gtc ttg gac cag aag caa	1433
Thr Ser Ser His Tyr Leu Gly Ser Leu Lys Val Leu Asp Gln Lys Gln	
395 400 405 410	
cca cgg aag cag agc cta gag cca gac aag gct gat cac ata agg gca	1481
Pro Arg Lys Gln Ser Leu Glu Pro Asp Lys Ala Asp His Ile Arg Ala	
415 420 425	
gct gtt tat cag gag tgg tta gaa aag aaa aat gtg tat tta cat gaa	1529
Ala Val Tyr Gln Glu Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu	
430 435 440	
atg cac aga ata aaa aga att gaa agc gaa aac ttg agg atc caa aat	1577
Met His Arg Ile Lys Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn	
445 450 455	
gaa cag aaa aaa gct gct aag aga gag gaa gcc ctg gca tca ttt gag	1625
Glu Gln Lys Lys Ala Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu	
460 465 470	
gcc tgg aag gca atg aaa gag aag gaa gca aag aga ata gct gca aaa	1673
Ala Trp Lys Ala Met Lys Glu Lys Glu Ala Lys Arg Ile Ala Ala Lys	
475 480 485 490	
aag agg ctg gag gaa aag aac aag aag aaa aca gaa gaa gaa aat gcc	1721
Lys Arg Leu Glu Glu Lys Asn Lys Lys Lys Thr Glu Glu Asn Ala	
495 500 505	
atg agg aaa ggc gag gcc ctg caa gca ttt gaa aaa tgg aaa gag aaa	1769
Met Arg Lys Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys	
510 515 520	
aag cta gaa tac ctc aaa gag aag acc agg agg gag aaa gaa tat gaa	1817
Lys Leu Glu Tyr Leu Lys Glu Lys Thr Arg Arg Glu Lys Glu Tyr Glu	
525 530 535	

aga gca aag aaa cag aaa gaa gag gaa gcg gtt gct gag aaa aag aaa	1865
Arg Ala Lys Lys Gln Lys Glu Glu Glu Ala Val Ala Glu Lys Lys Lys	
540 545 550	
gac agt tta act gct ttt gaa aaa tgg agt gag aga aag gaa gct ctc	1913
Asp Ser Leu Thr Ala Phe Glu Lys Trp Ser Glu Arg Lys Glu Ala Leu	
555 560 565 570	
ctc aag caa aag gag aag gag aaa ata aat gag aga aag gaa gag	1961
Leu Lys Gln Lys Glu Lys Glu Lys Ile Asn Glu Arg Arg Lys Glu Glu	
575 580 585	
ctg aag aga gcc gag aag aaa gac aaa gac aag caa gcc atc agt gaa	2009
Leu Lys Arg Ala Glu Lys Lys Asp Lys Asp Lys Gln Ala Ile Ser Glu	
590 595 600	
tac gaa aag tgg ctg gaa aag aaa gaa agg caa gaa aga att gaa cgg	2057
Tyr Glu Lys Trp Leu Glu Lys Lys Glu Arg Gln Glu Arg Ile Glu Arg	
605 610 615	
aaa cag aag aag cgc cac tcc ttc ctt gag agc gag aca cac cca cca	2105
Lys Gln Lys Lys Arg His Ser Phe Leu Glu Ser Glu Thr His Pro Pro	
620 625 630	
tgg agt cct ccg agc aga act gcg ccc tca aaa gta ttt tga	2147
Trp Ser Pro Pro Ser Arg Thr Ala Pro Ser Lys Val Phe	
635 640 645	
tgtttctggc tcttgatttt ttttcagtt caccaactgt actcatggat taaaaacgag	2207
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gcatgaaaga gatacttgc agttaatca gtggaaacat tttctgaagt gtcctcatca	2327
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gcttc tagag tgttagttgg gcattgaagg tccctggaga ccatggcat gttatcttt	2567
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gttgaggcca cagaactcta gtcagtcact ttagtaaaga actttgccat agggtttaat	2687
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<210> 46	
<211> 647	
<212> PRT	
<213> Mus musculus	

<400> 46
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 20 25 30
 Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
 35 40 45
 Asp Ser Asp Glu Ile Val Ser Leu Gly Glu Phe Ser Asp Thr Ser Thr
 50 55 60
 Asp Glu Ser Leu Val Arg Lys Lys Met Asn Asp Phe His Ile Ser Asp
 65 70 75 80
 Asp Glu Glu Lys Asn Ser Pro Arg Leu Ser Phe Leu Lys Thr Lys Lys
 85 90 95
 Val Asn Arg Ala Ile Ser Asn Asp Ala Leu Asp Ser Ser Thr Pro Gly
 100 105 110
 Ser Glu Gly Ser Ser Pro Asp Ala Gln Glu Asp Val Thr Gly Asp Ser
 115 120 125
 Leu Pro Lys Ser Gln Asn Asp Asp Arg Glu Val Gly Arg Glu Ile Ile
 130 135 140
 Thr Val Lys Pro Thr Pro Arg Met His Pro Val Lys Arg Ser Thr Ser
 145 150 155 160
 Ser Gly Glu Thr Ser Ser Gly Leu Asp Ala Asp Gly His Phe Lys Pro
 165 170 175
 Ser Pro Gln Pro Arg Ser Met Leu Lys Lys Ser Ser His Thr Glu Glu
 180 185 190
 Gly Val Arg Pro Gly Val Asp Lys Glu His Ser Ile Ser Glu Ala Ser
 195 200 205
 Ala Pro Thr Pro Ser Leu Pro Arg Gln Asn Gly Thr Glu Leu Gln Thr
 210 215 220
 Glu Glu Lys Ile Tyr Ser Glu Asn Leu Asp Leu Glu Asp Ser Leu Leu
 225 230 235 240
 Gln Ser Leu Thr Ser Ser Ser Phe Lys Glu Ser Pro Gly Gly Cys Thr
 245 250 255
 Ser Pro Gly Ser Gln Glu Lys Val Pro Ile Lys Asp His Asp Gly Glu
 260 265 270
 Pro Thr Glu Ile Trp Asp Ser Leu Leu Ser Asn Glu Asn Glu Gly Ser
 275 280 285
 Ser Val Leu Val Asn Cys Val Thr Pro Glu Leu Glu Gln Pro Lys Asp
 290 295 300

Gly Gln Val Ala Ala Asp Asp Leu Glu Glu Glu Arg Glu Lys Gly Gly
 305 310 315 320

Phe Thr Glu Asp Asp Leu Thr Thr Asp Pro Leu Leu Ser Thr Ser Pro
 325 330 335

Ser Val Ile Thr Pro Thr Glu Pro Ala Glu Pro Ala Lys Lys Ala Asn
 340 345 350

Glu Asp Arg Asn Thr Lys Asn Lys Lys Thr Thr Asn Asn Arg Val Ser
 355 360 365

Ser Ala Ser Gly Ser Arg Leu Met Thr Ser Glu Phe Leu Lys Arg Ser
 370 375 380

Gly Pro Thr Lys Arg Ser Pro Ser Ala Ala Thr Ser Ser His Tyr Leu
 385 390 395 400

Gly Ser Leu Lys Val Leu Asp Gln Lys Gln Pro Arg Lys Gln Ser Leu
 405 410 415

Glu Pro Asp Lys Ala Asp His Ile Arg Ala Ala Val Tyr Gln Glu Trp
 420 425 430

Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys Arg
 435 440 445

Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala Ala
 450 455 460

Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys Ala Met Lys
 465 470 475 480

Glu Lys Glu Ala Lys Arg Ile Ala Ala Lys Lys Arg Leu Glu Glu Lys
 485 490 495

Asn Lys Lys Lys Thr Glu Glu Asn Ala Met Arg Lys Gly Glu Ala
 500 505 510

Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Leu Glu Tyr Leu Lys
 515 520 525

Glu Lys Thr Arg Arg Glu Lys Glu Tyr Glu Arg Ala Lys Lys Gln Lys
 530 535 540

Glu Glu Glu Ala Val Ala Glu Lys Lys Lys Asp Ser Leu Thr Ala Phe
 545 550 555 560

Glu Lys Trp Ser Glu Arg Lys Glu Ala Leu Leu Lys Gln Lys Glu Lys
 565 570 575

Glu Lys Ile Asn Glu Arg Arg Lys Glu Glu Leu Lys Arg Ala Glu Lys
 580 585 590

Lys Asp Lys Asp Lys Gln Ala Ile Ser Glu Tyr Glu Lys Trp Leu Glu
 595 600 605

Lys Lys Glu Arg Gln Glu Arg Ile Glu Arg Lys Gln Lys Lys Arg His
 610 615 620

Ser Phe Leu Glu Ser Glu Thr His Pro Pro Trp Ser Pro Pro Ser Arg
 625 630 635 640

Thr Ala Pro Ser Lys Val Phe
 645

<210> 47
 <211> 647
 <212> PRT
 <213> Mus musculus

<400> 47
 Met Ser Asp Glu Ile Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
 1 5 10 15

Lys Ala Thr Lys Arg Thr Ser Phe Gln Asp Glu Leu Ile Arg Ala Ile
 20 25 30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
 35 40 45

Asp Ser Asp Glu Ile Val Ser Leu Gly Glu Phe Ser Asp Thr Ser Thr
 50 55 60

Asp Glu Ser Leu Val Arg Lys Lys Met Asn Asp Phe His Ile Ser Asp
 65 70 75 80

Asp Glu Glu Lys Asn Ser Pro Arg Leu Ser Phe Leu Lys Thr Lys Lys
 85 90 95

Val Asn Arg Ala Ile Ser Asn Asp Ala Leu Asp Ser Ser Thr Pro Gly
 100 105 110

Ser Glu Gly Ser Ser Pro Asp Ala Gln Glu Asp Val Thr Gly Asp Ser
 115 120 125

Leu Pro Lys Ser Gln Asn Asp Asp Arg Glu Val Gly Arg Glu Ile Ile
 130 135 140

Thr Val Lys Pro Thr Pro Arg Met His Pro Val Lys Arg Ser Thr Ser
 145 150 155 160

Ser Gly Glu Thr Ser Ser Gly Leu Asp Ala Asp Gly His Phe Lys Pro
 165 170 175

Ser Pro Gln Pro Arg Ser Met Leu Lys Lys Ser Ser His Thr Glu Glu
 180 185 190

Gly Val Arg Pro Gly Val Asp Lys Glu His Ser Ile Ser Glu Ala Ser
 195 200 205

Ala Pro Thr Pro Ser Leu Pro Arg Gln Asn Gly Thr Glu Leu Gln Thr
 210 215 220

Glu Glu Lys Ile Tyr Ser Glu Asn Leu Asp Leu Glu Asp Ser Leu Leu
 225 230 235 240

Gln Ser Leu Thr Ser Ser Ser Phe Lys Glu Ser Pro Gly Gly Cys Thr
 245 250 255

Ser Pro Gly Ser Gln Glu Lys Val Pro Ile Lys Asp His Asp Gly Glu
 260 265 270

Pro Thr Glu Ile Trp Asp Ser Leu Leu Ser Asn Glu Asn Glu Gly Ser
 275 280 285

Ser Val Leu Val Asn Cys Val Thr Pro Glu Leu Glu Gln Pro Lys Asp
 290 295 300

Gly Gln Val Ala Ala Asp Asp Leu Glu Glu Arg Glu Lys Gly Gly
 305 310 315 320

Phe Thr Glu Asp Asp Leu Thr Thr Asp Pro Leu Leu Ser Thr Ser Pro
 325 330 335

Ser Val Ile Thr Pro Thr Glu Pro Ala Glu Pro Ala Lys Lys Ala Asn
 340 345 350

Glu Asp Arg Asn Thr Lys Asn Lys Lys Thr Thr Asn Asn Arg Val Ser
 355 360 365

Ser Ala Ser Gly Ser Arg Leu Met Thr Ser Glu Phe Leu Lys Arg Ser
 370 375 380

Gly Pro Thr Lys Arg Ser Pro Ser Ala Ala Thr Ser Ser His Tyr Leu
 385 390 395 400

Gly Ser Leu Lys Val Leu Asp Gln Lys Gln Pro Arg Lys Gln Ser Leu
 405 410 415

Glu Pro Asp Lys Ala Asp His Ile Arg Ala Ala Val Tyr Gln Glu Trp
 420 425 430

Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys Arg
 435 440 445

Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala Ala
 450 455 460

Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys Ala Met Lys
 465 470 475 480

Glu Lys Glu Ala Lys Arg Ile Ala Ala Lys Lys Arg Leu Glu Glu Lys
 485 490 495

Asn Lys Lys Lys Thr Glu Glu Asn Ala Met Arg Lys Gly Glu Ala
 500 505 510

Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Leu Glu Tyr Leu Lys
 515 520 525

Glu Lys Thr Arg Arg Glu Lys Glu Tyr Glu Arg Ala Lys Lys Gln Lys
 530 535 540

Glu Glu Glu Ala Val Ala Glu Lys Lys Lys Asp Ser Leu Thr Ala Phe
 545 550 555 560

Glu Lys Trp Ser Glu Arg Lys Glu Ala Leu Leu Lys Gln Lys Glu Lys
 565 570 575

Glu Lys Ile Asn Glu Arg Arg Lys Glu Glu Leu Lys Arg Ala Glu Lys
 580 585 590

Lys Asp Lys Asp Lys Gln Ala Ile Ser Glu Tyr Glu Lys Trp Leu Glu
 595 600 605

Lys Lys Glu Arg Gln Glu Arg Ile Glu Arg Lys Gln Lys Lys Arg His
 610 615 620

Ser Phe Leu Glu Ser Glu Thr His Pro Pro Trp Ser Pro Pro Ser Arg
 625 630 635 640

Thr Ala Pro Ser Lys Val Phe
 645

<210> 48

<211> 344

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein sequence

<400> 48

Glu Ser Gln Val Thr Ala Asp Asp Leu Glu Glu Lys Ala Lys Ala
 1 5 10 15

Glu Leu Ile Met Asp Asp Asp Arg Thr Val Asp Pro Leu Leu Ser Lys
 20 25 30

Ser Gln Ser Ile Leu Ile Ser Thr Ser Ala Thr Ala Ser Ser Lys Lys
 35 40 45

Thr Ile Glu Asp Arg Asn Ile Lys Asn Lys Lys Ser Thr Asn Asn Arg
 50 55 60

Ala Ser Ser Ala Ser Ala Arg Leu Met Thr Ser Glu Phe Leu Lys Lys
 65 70 75 80

Ser Ser Ser Lys Arg Arg Thr Pro Ser Thr Thr Ser Ser His Tyr
 85 90 95

Leu Gly Thr Leu Lys Val Leu Asp Gln Lys Pro Ser Gln Lys Gln Ser
 100 105 110

Ile Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala Ala Val Tyr Gln Glu
 115 120 125

Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys
 130 135 140
 Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala
 145 150 155 160
 Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys Ala Met
 165 170 175
 Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys Lys Arg Leu Glu Glu
 180 185 190
 Lys Asn Lys Lys Thr Glu Glu Asn Ala Ala Arg Lys Gly Glu
 195 200 205
 Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Met Glu Tyr Leu
 210 215 220
 Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu Arg Ala Lys Lys Gln
 225 230 235 240
 Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys Asp Asn Leu Thr Ala
 245 250 255
 Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe Phe Lys Gln Lys Lys
 260 265 270
 Lys Glu Lys Ile Asn Glu Lys Arg Lys Glu Glu Leu Lys Arg Ala Glu
 275 280 285
 Lys Lys Asp Lys Asp Lys Gln Ala Ile Asn Glu Tyr Glu Lys Trp Leu
 290 295 300
 Glu Asn Lys Glu Lys Gln Glu Arg Ile Glu Arg Lys Gln Lys Lys Arg
 305 310 315 320
 His Ser Phe Leu Glu Ser Glu Ala Leu Pro Pro Trp Ser Pro Pro Ser
 325 330 335
 Arg Thr Val Phe Ala Lys Val Phe
 340

<210> 49
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 protein sequence

<400> 49
 Ser Gln Lys Gln Ser Ile Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala
 1 5 10 15

Ala Val Tyr Gln Glu Trp Leu Glu Lys Lys Asn Val Tyr Leu His Glu
 20 25 30

Met His Arg Ile Lys Arg Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn
 35 40 45

Glu Gln Lys Lys Ala Ala Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu
 50 55 60

Ala Trp Lys Ala Met Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys
 65 70 75 80

Lys Arg Leu Glu Glu Lys Asn Lys Lys Thr Glu Glu Glu Asn Ala
 85 90 95

Ala Arg Lys Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys
 100 105 110

Lys Met Glu Tyr Leu Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu
 115 120 125

Arg Ala Lys Lys Gln Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys
 130 135 140

Asp Asn Leu Thr Ala Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe
 145 150 155 160

Phe Lys Gln Lys Lys Glu Lys Ile Asn Glu Lys Arg Lys Glu Glu
 165 170 175

Leu Lys Arg Ala Glu Lys Lys Asp Lys Asp Lys Gln Ala Ile Asn Glu
 180 185 190

Tyr Glu Lys Trp Leu Glu Asn Lys Glu Lys Gln Glu Arg Ile Glu Arg
 195 200 205

Lys Gln Lys Lys Arg His Ser Phe Leu Glu Ser Glu Ala Leu Pro Pro
 210 215 220

Trp Ser Pro Pro Ser Arg Thr Val Phe Ala Lys Val Phe
 225 230 235

<210> 50

<211> 170

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein sequence

<400> 50

Ala Met Lys Glu Lys Glu Ala Lys Lys Ile Ala Ala Lys Lys Arg Leu
1 5 10 15Glu Glu Lys Asn Lys Lys Lys Thr Glu Glu Glu Asn Ala Ala Arg Lys
20 25 30

Gly Glu Ala Leu Gln Ala Phe Glu Lys Trp Lys Glu Lys Lys Met Glu
 35 40 45

Tyr Leu Lys Glu Lys Asn Arg Lys Glu Arg Glu Tyr Glu Arg Ala Lys
 50 55 60

Lys Gln Lys Glu Glu Glu Thr Val Ala Glu Lys Lys Lys Asp Asn Leu
 65 70 75 80

Thr Ala Val Glu Lys Trp Asn Glu Lys Lys Glu Ala Phe Phe Lys Gln
 85 90 95

Lys Lys Lys Glu Lys Ile Asn Glu Lys Arg Lys Glu Glu Leu Lys Arg
 100 105 110

Ala Glu Lys Lys Asp Lys Asp Lys Gln Ala Ile Asn Glu Tyr Glu Lys
 115 120 125

Trp Leu Glu Asn Lys Glu Lys Gln Glu Arg Ile Glu Arg Lys Gln Lys
 130 135 140

Lys Arg His Ser Phe Leu Glu Ser Glu Ala Leu Pro Pro Trp Ser Pro
 145 150 155 160

Pro Ser Arg Thr Val Phe Ala Lys Val Phe
 165 170

<210> 51

<211> 477

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
protein sequence

<400> 51

Met Ser Asp Glu Val Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
1 5 10 15

Lys Val Thr Lys Arg Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile
20 25 30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
35 40 45

Asp Ser Asp Glu Ile Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala
50 55 60

Asp Glu Asn Ser Val Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp
65 70 75 80

Asp Glu Glu Lys Asn Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys
85 90 95

Ser Asn Gly Asn Ile Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn
 100 105 110
 Glu Glu Glu Met Ala Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser
 115 120 125
 Phe Ser Glu Ser Gln Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile
 130 135 140
 Lys Met Lys Pro Lys Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser
 145 150 155 160
 Ala Glu Asn Asn Ser Leu Asp Thr Asp Asp His Phe Lys Pro Ser Pro
 165 170 175
 Trp Pro Arg Ser Met Leu Lys Lys Ser His Met Glu Glu Lys Asp
 180 185 190
 Gly Leu Glu Asp Lys Glu Thr Ala Leu Ser Glu Glu Leu Glu Leu His
 195 200 205
 Ser Ala Pro Ser Ser Leu Pro Thr Pro Asn Gly Ile Gln Leu Glu Ala
 210 215 220
 Glu Lys Lys Ala Phe Ser Glu Asn Leu Asp Pro Glu Asp Ser Cys Leu
 225 230 235 240
 Thr Ser Leu Ala Ser Ser Ser Leu Lys Gln Ile Leu Gly Asp Ser Phe
 245 250 255
 Ser Pro Gly Ser Glu Gly Asn Ala Ser Gly Lys Asp Pro Asn Glu Glu
 260 265 270
 Ile Thr Glu Asn His Asn Ser Leu Lys Ser Asp Glu Asn Lys Glu Asn
 275 280 285
 Ser Phe Ser Ala Asp His Val Thr Thr Ala Val Glu Lys Ser Lys Glu
 290 295 300
 Ser Gln Val Thr Ala Asp Asp Leu Glu Glu Lys Ala Lys Ala Glu
 305 310 315 320
 Leu Ile Met Asp Asp Asp Arg Thr Val Asp Pro Leu Leu Ser Lys Ser
 325 330 335
 Gln Ser Ile Leu Ile Ser Thr Ser Ala Thr Ala Ser Ser Lys Lys Thr
 340 345 350
 Ile Glu Asp Arg Asn Ile Lys Asn Lys Lys Ser Thr Asn Asn Arg Ala
 355 360 365
 Ser Ser Ala Ser Ala Arg Leu Met Thr Ser Glu Phe Leu Lys Lys Ser
 370 375 380
 Ser Ser Lys Arg Arg Thr Pro Ser Thr Thr Ser Ser His Tyr Leu
 385 390 395 400

Gly Thr Leu Lys Val Leu Asp Gln Lys Pro Ser Gln Lys Gln Ser Ile
 405 410 415

Glu Pro Asp Arg Ala Asp Asn Ile Arg Ala Ala Val Tyr Gln Glu Trp
 420 425 430

Leu Glu Lys Lys Asn Val Tyr Leu His Glu Met His Arg Ile Lys Arg
 435 440 445

Ile Glu Ser Glu Asn Leu Arg Ile Gln Asn Glu Gln Lys Lys Ala Ala
 450 455 460

Lys Arg Glu Glu Ala Leu Ala Ser Phe Glu Ala Trp Lys
 465 470 475

<210> 52

<211> 418

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 protein sequence

<400> 52

Met Ser Asp Glu Val Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
 1 5 10 15

Lys Val Thr Lys Arg Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile
 20 25 30

Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
 35 40 45

Asp Ser Asp Glu Ile Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala
 50 55 60

Asp Glu Asn Ser Val Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp
 65 70 75 80

Asp Glu Glu Lys Asn Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys
 85 90 95

Ser Asn Gly Asn Ile Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn
 100 105 110

Glu Glu Glu Met Ala Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser
 115 120 125

Phe Ser Glu Ser Gln Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile
 130 135 140

Lys Met Lys Pro Lys Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser
 145 150 155 160

Ala Glu Asn Asn Ser Leu Asp Thr Asp Asp His Phe Lys Pro Ser Pro
 165 170 175

Trp Pro Arg Ser Met Leu Lys Lys Ser His Met Glu Glu Lys Asp
 180 185 190
 Gly Leu Glu Asp Lys Glu Thr Ala Leu Ser Glu Glu Leu Glu Leu His
 195 200 205
 Ser Ala Pro Ser Ser Leu Pro Thr Pro Asn Gly Ile Gln Leu Glu Ala
 210 215 220
 Glu Lys Lys Ala Phe Ser Glu Asn Leu Asp Pro Glu Asp Ser Cys Leu
 225 230 235 240
 Thr Ser Leu Ala Ser Ser Ser Leu Lys Gln Ile Leu Gly Asp Ser Phe
 245 250 255
 Ser Pro Gly Ser Glu Gly Asn Ala Ser Gly Lys Asp Pro Asn Glu Glu
 260 265 270
 Ile Thr Glu Asn His Asn Ser Leu Lys Ser Asp Glu Asn Lys Glu Asn
 275 280 285
 Ser Phe Ser Ala Asp His Val Thr Thr Ala Val Glu Lys Ser Lys Glu
 290 295 300
 Ser Gln Val Thr Ala Asp Asp Leu Glu Glu Glu Lys Ala Lys Ala Glu
 305 310 315 320
 Leu Ile Met Asp Asp Asp Arg Thr Val Asp Pro Leu Leu Ser Lys Ser
 325 330 335
 Gln Ser Ile Leu Ile Ser Thr Ser Ala Thr Ala Ser Ser Lys Lys Thr
 340 345 350
 Ile Glu Asp Arg Asn Ile Lys Asn Lys Ser Thr Asn Asn Arg Ala
 355 360 365
 Ser Ser Ala Ser Ala Arg Leu Met Thr Ser Glu Phe Leu Lys Lys Ser
 370 375 380
 Ser Ser Lys Arg Arg Thr Pro Ser Thr Thr Ser Ser His Tyr Leu
 385 390 395 400
 Gly Thr Leu Lys Val Leu Asp Gln Lys Pro Ser Gln Lys Gln Ser Ile
 405 410 415
 Glu Pro

<210> 53
 <211> 303
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 protein sequence

<400> 53
 Met Ser Asp Glu Val Phe Ser Thr Thr Leu Ala Tyr Thr Lys Ser Pro
 1 5 10 15
 Lys Val Thr Lys Arg Thr Thr Phe Gln Asp Glu Leu Ile Arg Ala Ile
 20 25 30
 Thr Ala Arg Ser Ala Arg Gln Arg Ser Ser Glu Tyr Ser Asp Asp Phe
 35 40 45
 Asp Ser Asp Glu Ile Val Ser Leu Gly Asp Phe Ser Asp Thr Ser Ala
 50 55 60
 Asp Glu Asn Ser Val Asn Lys Lys Met Asn Asp Phe His Ile Ser Asp
 65 70 75 80
 Asp Glu Glu Lys Asn Pro Ser Lys Leu Leu Phe Leu Lys Thr Asn Lys
 85 90 95
 Ser Asn Gly Asn Ile Thr Lys Asp Glu Pro Val Cys Ala Ile Lys Asn
 100 105 110
 Glu Glu Glu Met Ala Pro Asp Gly Cys Glu Asp Ile Val Val Lys Ser
 115 120 125
 Phe Ser Glu Ser Gln Asn Lys Asp Glu Glu Phe Glu Lys Asp Lys Ile
 130 135 140
 Lys Met Lys Pro Lys Pro Arg Ile Leu Ser Ile Lys Ser Thr Ser Ser
 145 150 155 160
 Ala Glu Asn Asn Ser Leu Asp Thr Asp Asp His Phe Lys Pro Ser Pro
 165 170 175
 Trp Pro Arg Ser Met Leu Lys Lys Ser His Met Glu Glu Lys Asp
 180 185 190
 Gly Leu Glu Asp Lys Glu Thr Ala Leu Ser Glu Glu Leu Glu Leu His
 195 200 205
 Ser Ala Pro Ser Ser Leu Pro Thr Pro Asn Gly Ile Gln Leu Glu Ala
 210 215 220
 Glu Lys Lys Ala Phe Ser Glu Asn Leu Asp Pro Glu Asp Ser Cys Leu
 225 230 235 240
 Thr Ser Leu Ala Ser Ser Ser Leu Lys Gln Ile Leu Gly Asp Ser Phe
 245 250 255
 Ser Pro Gly Ser Glu Gly Asn Ala Ser Gly Lys Asp Pro Asn Glu Glu
 260 265 270
 Ile Thr Glu Asn His Asn Ser Leu Lys Ser Asp Glu Asn Lys Glu Asn
 275 280 285
 Ser Phe Ser Ala Asp His Val Thr Thr Ala Val Glu Lys Ser Lys
 290 295 300